This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

Claims 1-12: (canceled).

Claim 13 (currently amended) A method for predicting resistance of ~~a pathogen~~human deficiency virus type 1 (HIV-1) to a therapeutic agent comprising:

(a) providing a neural network;

(b) training a neural network on a training data set, wherein each member of the training data set corresponds to a genetic mutation that correlates to a phenotypic change that causes a change in therapeutic resistance of ~~the pathogen~~HIV-1, said training being performed by

i) propagating a training data set in a feed-forward fashion,

ii) calculating the associated error,

iii) back propagating the error,

iv) adjusting the weights in the neural network,

v) minimizing the error function by repeating the steps i), ii), iii), iv),

vi) ~~using~~inputting a testing data set to ensure proper training, said testing data set comprising members that correspond to at least one genetic mutation, the presence of which correlates to ~~that correlate to~~ a phenotypic change that cause a change in resistance of ~~pathogen~~HIV-1 to at least one therapeutic agent, which testing data set is different from the training data set:

(c) providing a determined HIV-1 genetic sequence from a patient ~~said pathogen;~~ by

i) obtaining [a]an HIV-1 sample from ~~said pathogen~~ the patient,

ii) obtaining the genetic sequence from the HIV-1 sample; and

d) predicting resistance of ~~the pathogen~~HIV-1 to the therapeutic agent by inputting the determined genetic sequence into the trained neural network which computes the predicted resistance of HIV-1 to a therapeutic agent.

Claim 14-17: (canceled)

Claim 18 (original): The method of claim 13, wherein the neural network is a three-layer feed-forward neural network.

Claim 19 (original): The method of claim 18, wherein the three-layer feed forward network comprises:

(a) a set of input nodes, wherein each member of the set of input nodes corresponds to a mutation in the genome of the pathogen;

(b) a plurality of hidden nodes; and

(c) a set of output nodes, wherein each member of the set of output nodes corresponds to a therapeutic agent used to treat the pathogen.

Claims 20-29: (canceled)